

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: January 16, 2003, 16:39:12, Search time 17.4857 seconds
(without alignments)
28.464 Million cell updates/sec

Title: US-09-856-070-21
Perfect score: 60
Sequence: 1 ERLMRLQDYR 12

Scoring table: BLAST62
Gapop 10 0, Gapext 0 5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100	0	580	P1976 bos taurus
2	60	100	0	585	P15311 homo sapien
3	57	95	0	585	P26040 mus musculus
4	44	73.3	886	1	KAS50 SALAC
5	39	65	0	495	P12414 homo sapien
6	39	65	0	880	P40047 saccharomyc
7	38	63	3	715	P40047 saccharomyc
8	37	61.7	303	1	P37599 bacillus su
9	37	61.7	756	1	P75154 homo sapien
10	37	61.7	1005	1	P58718 metracoccus
11	37	61.7	2472	1	P13813 homo sapien
12	37	61.7	2472	1	P16086 rattus norv
13	37	61.7	2477	1	P07751 gallus gall
14	36	60	0	320	P15311 homo sapien
15	36	60	0	365	P40047 saccharomyc
16	36	60	0	880	P40047 saccharomyc
17	36	60	0	892	P12814 homo sapien
18	36	60	0	892	P12814 homo sapien
19	36	60	0	1108	P40047 saccharomyc
20	35	59.2	550	1	P08659 photinus py
21	35	58.3	224	1	P08659 photinus py
22	35	58.3	519	1	P40047 saccharomyc
23	35	58.3	576	1	P40047 saccharomyc
24	35	58.3	576	1	P40047 saccharomyc
25	35	58.3	583	1	P26040 mus musculus
26	35	58.3	583	1	P26040 mus musculus
27	35	58.3	583	1	P26040 mus musculus
28	35	58.3	721	1	P40047 saccharomyc
29	35	58.3	721	1	P40047 saccharomyc
30	35	58.3	721	1	P40047 saccharomyc
31	35	58.3	891	1	P40047 saccharomyc
32	35	58.3	891	1	P40047 saccharomyc
33	35	58.3	964	1	P40047 saccharomyc

ALIGNMENTS

RESULT 1

1	ERL_HOVIN	STANDARD	PRT	580 AA.
AC	F31976;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	16 OCT 2001 (Rel. 40, Last annotation update)			
DE	Ervin (p81) (Cytovillin) (Villin 2).			
GN	Vill2.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RA	Bergson C.M., Zhao H., Salih K., Duman P.S., Nestler E.J.;			
RT	"Ervin and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus";			
RI	Mol. Cell. Neurosci. 4:64-73(1993).			
RN	[2]			
RP	SEQUENCE OF 1-15 AND 126-140.			
RP	TISSUE=Kidney;			
RA	MEDLINE=96231337; PubMed=8660651;			
RA	Gallat A., Gebard M.C., Houet F., Riviere S.;			
PT	"Proteins and their amino acid compositions: uniqueness, variability, and applications";			
PL	Arch Biochem Biophys. 330:229-237(1996).			
CC	1-15 PUNTIEN: PE-EARLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE.			
CC	1-15 SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE. PROTEIN (CYTOSOLASMIC SIDE).			
CC	1-15 PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.			
CC	1-15 SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.			
CC	THIS SWISS-PROT entry is deprecated. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Source by and for commercial entities requires a license agreement (see http://www.isb.sib.ch/announce/ or send an email to license@isb.sib.ch).			
CC	EMBL: M98498; AAA00510.1; -			
DR	InterPro: IPR000299, Band_4.1.			
DR	InterPro: IPR000299, Ez/raf/moesin.			
DR	Pfam: PF00379; Band_4.1; 1.			
DR	Pfam: PF00769; ERM; 1.			
DR	PRINTS: PR00935; HAND41.			
DR	SMART: SM00295; H41; 1.			
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DR	PROSITE			

CC -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
CC EPITHELIAL CELLS.
CC -1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL: X60671; CAA43086.1; -
CC PIR: B41129; B41129.
CC MGD: MGI:96931; V112.
CC InterPro: IPR000239; Band_4.1.
CC InterPro: IPR000798; P7/rad/moesin.
CC Pfam: PF0373; Band_4.1; 1.
CC Pfam: PF00769; PPM; 1.
CC PRINTS: SM00395; BAND4.
CC SMART: SM00245; B41; 1.
CC PROSITE: PS00660; BAND_4.1.1; 1.
CC PROSITE: PS00661; BAND_4.1.2; 1.
CC PROSITE: PS00657; BAND_4.1.3; 1.
CC
CC Structural protein: Cytoskeleton, Phosphorylation.
CC INIT_MET 0 0 BY SIMILARITY.
CC FT DOMAIN 57 224 BAND 4.1-LIKE.
CC FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR)
CC FT MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
CC FT MOD_RES 353 353 PHOSPHORYLATION (BY SIMILARITY).
CC FT SEQUENCE 585 AA; 69214 MW; 2057E7E2E2B0C5D2 CRC64.
CC
CC Query Match 95.9% Score 57. DB 1; Length 585;
CC Best local Similarity 91.7%; Pred. No. 0.0092;
CC Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 EELMLRLQDYEE 12
CC DB 344 EELMLRLQDYEQ 355
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CC RESULT 4
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CC ID RAS50_SULAC STANDARD; PPT; 886 AA
CC AC 033600;
CC DT 16-OCT-2001 (Rel. 40. Created)
CC DI 16-OCT-2001 (Rel. 40. Last sequence update)
CC DI 16-OCT-2001 (Rel. 40. Last annotation update)
CC DE DNA double-strand break repair rad50 ATPase.
CC GN RAD50.
CC OS Sulfolobus acidocaldarius.
CC OC Archaea; Eubacteria; Thermoprotei; Sulfolobales; Sulfolobaceae;
CC CC Sulfolobus
CC OX NCBI_TaxID=2285;
CC [1]
CC SEQUENCE FROM N.A.
CC RAIN-ATC 3496 / N114 1176 / LSM 636;
CC MEDLINE=97362314; PubMed=921174;
CC Elie C., Haucher M.F., Fondrat C., Forterre P.;
CC "A protein related to eucaryal and bacterial DNA-motor proteins in the
CC hyperthermophilic archaeon Sulfolobus acidocaldarius".
CC J Mol Evol 45:107-114(1997)
CC
CC -1- FUNCTION: Involved in DNA double strand break repair (DSBP). The
CC rad50/mre11 complex possesses single strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
CC and/or repositioning DNA ends into the mre11 active site (By
CC similarity).
CC -1- SUBUNIT: Forms a complex with mre11 (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY
CC

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CC
CC EMBL: Y10687; CAA71688.1; -
CC InterPro: IPR003439; ABC_Transportr.
CC InterPro: IPR003395; SMC_N.
CC Pfam: PF02463; SMC_N; 1.
CC Pfam: PF000006; ABC_Transportr; 1.
CC PRODOM: P000006; ABC_Transportr; Coiled coil.
CC DNA repair; Hydrolyase; ATP-binding; Coiled coil.
CC NP_BIND 30 37 ATP (BY SIMILARITY).
CC FT DOMAIN 174 727 COILED COIL (POTENTIAL).
CC SEQUENCE 586 AA; 104857 MW; 0390AE1403194104 CRC64;
CC
CC Query Match 73.3% Score 44; DB 1; Length 886;
CC Best local Similarity 66.7%; Pred. No. 3.2;
CC Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 EELMLRLQDYEE 12
CC DB 258 EELMLRLQDYEE 269
CC
CC RESULT 5
CC FUT4_HUMAN
CC ID FUT4_HUMAN STANDARD; PPT; 405 AA.
CC AC P22083;
CC DT 01-AUG-1991 (Rel. 19. Created)
CC DI 01-OCT-1996 (Rel. 34. Last sequence update)
CC DI 15-JUN-2002 (Rel. 41. Last annotation update)
CC DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.1) (Glycoside 4-L-
CC fucosyltransferase) (Fucosyltransferase 4) (FUT-IV) (ELAM-1 ligand
CC fucosyltransferase).
CC GN FUT4 OR ELF1.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE=Peripheral blood leukocytes;
CC MEDLINE=91084863; PubMed=1716430;
CC Lowe J.B., Kukowska-Latallo J.F., Nair R.P., Larsen R.D., Marks R.M.,
CC Macher B.A., Kelly R.J., Ernst L.K.;
CC "Molecular cloning of a human fucosyltransferase gene that determines
CC expression of the Lewis x and VIM-2 epitopes but not ELAM-1-dependent
CC cell adhesion".
CC J Biol Chem 266:17457-17477(1991).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE=91084863; PubMed=1702034;
CC Sack S.L., Hession C., Jeff D., Griffiths B., Lizard P., Newman R.,
CC Chi-Rosso G., Lohb R.;
CC "ELF1: a gene that directs the expression of an ELAM-1 ligand".
CC Cell 63:1349-1356(1990).
CC [3]
CC SEQUENCE OF 1-400 FROM N.A.
CC MEDLINE=92044084; PubMed=1718983;
CC Kumar P., Polvin B., Muller W.A., Stanley P.;
CC "Cloning of a human alpha(1,3) fucosyltransferase gene that encodes
CC ELT but does not confer ELAM-1 recognition on Chinese hamster ovary
CC cell transfectants".
CC J Biol Chem 266:21777-21783(1991).
CC -1- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED IN
CC THE EXPRESSION OF LEWIS X/SSEA-1 AND VIM-2 ANTIGENS.
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
CC FORM IN TRANS CIS/ENAP OF COLG1.
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

AC p37549.
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chemotaxis protein chev.
 CN CHEV.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1423;
 RN SEQUENCE FROM N.A.
 RP STRAIN-168;
 RC MEDLINE=94222854; PubMed=9169223;
 RX Frederick K.L., Helmann J.D.;
 FT "Local chemotaxis signaling pathways in Bacillus subtilis: a sigma D-
 RT dependent gene encodes a novel protein with both CheW and CheY
 RT homologous domains."
 PL J. Bacteriol. 176:2727-2735(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-168;
 RC Scanlan E., Devine K.M.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/EBI databases.
 RP SEQUENCE FROM N.A.
 RP STRAIN-168;
 RX MEDLINE=94244034; PubMed=949477;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherdt S.,
 RA Borriss R., Hoursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Gaidwell H., Capuano V., Carter N.M.,
 RA Choi S.K., Codanis J.J., Conneron J.P., Cummings N.J., Daniel R.A.,
 RA Denoit F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Erington J., Fahren C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 RA Gim S.Y., Glaser P., Goffeau A., Gollightly F.J., Grandi G.,
 RA Guisepi G., Guy H.J., Hada K., Haech J., Harwood C.P., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Bianchini M., Klein C.,
 RA Kobayashi Y., Koertge P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidos A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maupel C., Modique C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogasawa K., Ogilvie A., Oshida R., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Pirzelle R., Papoport G., Pey M., Reynolds S.,
 RA Plegier M., Pivoli C., Pocha E., Poche S., Pocha M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Sciffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin H.S., Soldo R.,
 RA Sorokin A., Tacconi F., Takan T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tozzoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis".
 PI Nature 390:240-256(1997)
 RN [4]
 RN FUNCTION.
 RP STRAIN-168 / 011085;
 PX MEDLINE=94222855; PubMed=949224.
 RA Rosario M.M.L., Erickson K.L., Ordal G.W., Helmann J.D.;
 RT "Chemotaxis in Bacillus subtilis requires either of two functionally
 RT redundant CheW homologs."
 RL J. Bacteriol. 176:2716-2726(1994).
 CC -!- FUNCTION: CHEMOTAXIS INVOLVES BOTH A PHOSPHORYLATION-DEPENDENT
 CC EXCITATION AND A METHYLATION-DEPENDENT ADAPTATION. CHEW AND CHEW
 CC FUNCTION TOGETHER TO COUPLE CHEA ACTIVATION TO METHYL-ACCEPTING
 CC CHEMOTAXIS PROTEIN RECEPTOR STATUS AND POSSIBLE CHEA-DEPENDENT
 CC PHOSPHORYLATION OF CHEW CONTRIBUTES TO ADAPTATION
 CC -!- DEVELOPMENTAL STAGE: PHA EXPRESSION IS SEEN IN EARLY STATIONARY
 CC PHASE.
 CC

CC -!- ITEM: PHOSPHORYLATED BY CHEA (POTENTIAL).
 CC -!- SIMILARITY: CONTAINS 1 CHEW DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC
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 CC
 CC EMBL: Z29584, CAA82701.1;
 CC EMBL: U05345; AAA16526.1;
 CC EMBL: AJ22587; CAA10864.1;
 CC EMBL: Z99111; CAB13274.1;
 CC PIP: S41419; S41419.
 CC Subtilist, RGL0923; chev.
 CC InterPro: IPR002545; Chev.
 CC InterPro: IPR001789; Response_reg.
 CC Pfam: PF00072; Response_reg.1.
 CC Pfam: PF01584; chev.1.
 CC ProDom: PD000039; Response_reg.1.
 CC SMART: SM00260; chev.1.
 CC SMART: SM00448; REC.1.
 CC PROSITE: PS00110; RESPONSE REGULATORY; 1.
 CC CHEW: CHEW; 153
 CC DOMAIN 14 302
 CC MOD_RES 50 50
 CC PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC SEQUENCE 305 AA; 3455 MW; 76094.450 C40D18 C6064;
 Query Match 61.7%, Score 37, EB 1, Length 303;
 Best Local Similarity 58.3%; Pred. No. 18;
 Matches 7, Conservative 3, Mismatches 2, Indels 0, Gaps 0;
 07 1 HELMLKLDYER 12
 13111:1111;
 Db 136 EDLMIFLDYER 147
 RESULT 9
 EFER_HUMAN
 ID EFER_HUMAN SLANARU; PRI; 75% AA.
 AC Q75154; Q9N010; Q9HIG0; Q9H155;
 DT 15-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Eferin.
 CN KIAA0665.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21486406; PubMed=11481332;
 RA Fricke E., Davies J.M., Scheller R.H.;
 RT "Identification of a novel Rab11/25 binding domain present in eferin
 RT and rip proteins."
 PL J. Biol. Chem. 276:38956-38959(2001).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K., Nagase T., Sugama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Chara G.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 PI INA Res. 5:169-176(1998).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP

RA MEDLINE-21096910; PubMed 11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Hicks D.K.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:349-352(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wallis J., Lloyd C., Hall R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBMIT: Bands to KABIL and RAD25.
 CC -1- SIMILARITY: CONTAINS 2 EF HAND CALCIUM-BINDING DOMAINS.
 CC
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 DR EMBL: AF495731; AAL12940.1;
 DR EMBL: AB014565; BAA31040.1;
 DR EMBL: AE006463; AAK61232.1;
 DR EMBL: AL024881; CAB92745.1;
 DR EMBL: AL049542; CAC17519.1;
 DR EMBL: Z98882; CAC17523.1;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 215 225 EF HAND 1 (POTENTIAL).
 FT CA_BIND 247 258 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 756 AA; 82439 MW; 26431339528AFB9 CRC64;

Query Match 61.7%; Score 37; DB 1; Length 756;
 Best Local Similarity 70.0%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EELMERLOQYEE 10
 III I I I I I I
 Db 728 EELMERLOQYEE 747

RESULT 10
 RA50_MELJA STANDARD; PRI: 1005 AA.
 AC Q58718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA double-strand break repair rad50 Afpase.
 GN RAD50 OR MJ1322.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-1A1-1 / DSM 2661 / AF04 43067;
 RC MEDLINE-96347999; PubMed-8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake T.A., Finkbeiner S.M., Clayton R.A., Gocayne J.D.,
 RA Kerec A.R., Dougherty B.A., Tomb J.P., Adams M.D., Reich C.L.,
 RA O'Leary A.L., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Goodenough N.S.M., Weidman T.F., Fuhmann T.I., Nguyen D.,
 RA Unterbach T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Burst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RC "Complete genome sequence of the methanococcal archaeon, Methanococcus
 RC jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The

rad50/mrell complex possesses single-strand endonuclease activity
 and ATP dependent double-strand-specific exonuclease activity.
 rad50 provides an ATP-dependent control of mrell activity by unwinding
 and/or repositioning DNA ends into the mrell active site (By
 similarity).
 CC -1- SUBMIT: Forms a complex with mrell (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY, RAD50 SUBFAMILY.
 CC
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 CC
 DR EMBL: U67572; AAR99331.1;
 DR TIGR: MJ1322;
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N; 1.
 DR Pfam: PF02483; SMC_C; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR DNA repair, Hydrolase, ATP binding; Coiled coil; Complete proteome.
 FT NP_BIND 32 39 ATP (BY SIMILARITY).
 FT DOMAIN 158 849 COILED COIL (POTENTIAL).
 SQ SEQUENCE 1005 AA; 119387 MW; 9888481734788F3 CRC64;
 Query Match 61.7%; Score 37; DB 1; Length 1005;
 Best Local Similarity 58.3%; Pred. No. 66;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EELMERLOQYEE 12
 III I I I I I I I
 Db 574 EELMERLOQYEE 585

RESULT 11
 SPEN_HUMAN STANDARD; PRI: 2472 AA.
 AC Q13813; Q16005; Q9P0V0; Q13186;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
 DE (Alpha I; spectrin) (Fodrin alpha chain).
 GN SPTAN1 OR SPTA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-90170946; PubMed-2307671;
 RA Moon R.T., McMahon A.P.;
 RT "Generation of diversity in nonerythroid spectrins. Multiple
 RT polypeptides are predicted by sequence analysis of cDNAs encompassing
 RT the coding region of human nonerythroid alpha-spectrin.";
 RL J. Biol. Chem. 265:4427-4433(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE: fetal brain;
 RA Clandi C.D., Morrow J.S.;
 RT "Complete cDNA sequence of human alpha I1 fetal brain spectrin.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 676-1595 FROM N.A.
 RC TISSUE: lung;
 RA MEDLINE-88983942; PubMed-2691949;
 RA McMahon A.P., Moon R.T.;
 RT "Structure and evolution of a non-erythroid spectrin, human
 RT alpha-Iodrin.";

Biochem. Soc. Trans. 15:804-807(1987).
 [4] SEQUENCE OF 676-1595 FROM N.A.
 RX MEDLINE-R7277023; PubMed-3038643;
 RA McMahon A.P., Giebelhaus D.H., Champion T.E., Bailey T.A., Jacey S.,
 Carritt B., Henchman S.K., Moon K.T.;
 RT "cDNA cloning, sequencing and chromosome mapping of a non-erythroid
 spectrin, human alpha-fodrin.";
 RL Differentiation 34:68-78(1987)
 [5] ERRATUM.
 RA McMahon A.P., Giebelhaus D.H., Champion J.E., Bailey J.A., Jacey S.,
 Carritt B., Henchman S.K., Moon K.T.;
 RL Differentiation 34:241-241(1987).
 [6] SEQUENCE OF 811-1529 FROM N.A. VARIANT ILE-1300, AND MUTAGENESIS
 RC TISSUE-Fetal brain;
 RX MEDLINE-97140462; PubMed-8993318;
 RA Stabach P.F., Glanville C.D., Claretz S.B., Chaly N., Morrow J.S.,
 RT "Site directed mutagenesis of alpha II spectrin at codon 1175
 modulates its mu-calpain susceptibility.";
 RL Biochemistry 36:57-65(1997)
 [7] SEQUENCE OF 1073-1349 FROM N.A.
 RA Murakami N., Speed W.C., Soeman M.I., Zychowski P.L., Wotterberg L.,
 Bakstis A.J., Kidd J.P., Kidd K.K.;
 RT "Association and linkage analyses of the non-erythroid alpha-spectrin
 (SPTAN1) gene on chromosome 9q34 with a large Swedish kindred.";
 RL submitted (MAY-1996) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
 INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
 THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
 CYTOSKELETON AT THE MEMBRANE
 CC -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 TETRAMERS
 CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN
 CC -!- SIMILARITY: CONTAINS 23 SPECTRIN REPEATS.
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 CC
 DR EMBL: J05243; AAA51790.1;
 DR EMBL: U83867; AAB41498.1;
 DR EMBL: M24773; AAA52468.1;
 DR EMBL: M18627; AAA51702.1;
 DR EMBL: U26396; AAF60364.1;
 DR EMBL: AF148808; AAF26672.1;
 DR HSSP: P07751; 1AFY.
 DR Genew: HGNP-11273; SPTAN1.
 DR MIM: 162810.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00036; efhand; 4.
 DR Pfam: PF00435; Spectrin; 32.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD0000012; EF-hand; 1.
 DR ProDom: PD0000066; SH3; 1.
 DR SMART: SM00054; EFh; 2.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00150; SPC; 20.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS50003; SH3; 1.
 KW Cytoskeleton; Membrane, Calmodulin-binding, Actin-binding;

KW Capping protein; Calcium-binding; Repeat; SH3 domain; Polymorphism.
 FT REPEAT 1 10 42 SPECTRIN 1.
 FT REPEAT 2 44 147 SPECTRIN 2.
 FT REPEAT 3 149 253 SPECTRIN 3.
 FT REPEAT 4 255 359 SPECTRIN 4.
 FT REPEAT 5 361 465 SPECTRIN 5.
 FT REPEAT 6 467 571 SPECTRIN 6.
 FT REPEAT 7 573 676 SPECTRIN 7.
 FT REPEAT 8 678 782 SPECTRIN 8.
 FT REPEAT 9 784 888 SPECTRIN 9.
 FT REPEAT 10 890 955 SPECTRIN 10.
 FT DOMAIN 967 1026 SH3.
 FT REPEAT 1062 1089 SPECTRIN 11.
 FT REPEAT 1091 1161 SPECTRIN 12.
 FT REPEAT 1208 1231 SPECTRIN 13.
 FT REPEAT 1233 1327 SPECTRIN 14.
 FT REPEAT 1339 1443 SPECTRIN 15.
 FT REPEAT 1445 1549 SPECTRIN 16.
 FT KATA 1551 1656 SPECTRIN 17.
 FT REPEAT 1658 1762 SPECTRIN 18.
 FT REPEAT 1764 1868 SPECTRIN 19.
 FT REPEAT 1870 1974 SPECTRIN 20.
 FT REPEAT 1976 2081 SPECTRIN 21.
 FT REPEAT 2091 2195 SPECTRIN 22.
 FT REPEAT 2205 2310 SPECTRIN 23.
 FT CA_BIND 2336 2347 EF_HAND 1 (POTENTIAL).
 FT SITE 2379 2392 EF_HAND 2 (POTENTIAL).
 FT VARIANT 1176 1177 CLEAVAGE (BY MU-CALPAIN).
 FT 1300 T->I.
 FT /FTID-VAR-012227.
 FT CONFLICT 150 150 N->K (IN REF. 2).
 FT CONFLICT 498 498 F->S (IN REF. 2).
 FT CONFLICT 737 737 V->I (IN REF. 2).
 FT CONFLICT 1586 1586 Q->QLSKL (IN REF. 2).
 FT CONFLICT 1595 1595 F->P (IN REF. 3 AND 4).
 FT CONFLICT 1625 1625 N->S (IN REF. 2).
 FT CONFLICT 1670 1671 IA->FD (IN REF. 2).
 FT CONFLICT 1918 1918 A->D (IN REF. 2).
 FT CONFLICT 2347 2348 DG->EF (IN REF. 2).
 FT CONFLICT 2448 2448 I->Y (IN REF. 2).
 SQ SEQUENCE 2472 AA; 284279 MW; 61.7% Score 37, DA 13, length 2472;
 Query Match 61.7%, Score 37, DA 13, length 2472;
 Best Local Similarity 58.38; Prod No. 1.8e+02;
 Mismatches 7, Conservative 3, Mismatches 2, Indels 0, Gaps 0;
 QY 1 EELMLRQDYEE 12
 DB 969 KRLVLAIVDYQE 980
 RESULT 12
 SPCN_RAT
 ID SPCN_RAT STANDARD; PRI: 2472 AA.
 AC P16086; P70477; O88663;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non erythroid alpha chain)
 DE (Alpha-II spectrin) (Fodrin alpha chain).
 GN SPTAN1 OR SPTA2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar; ISSUE Liver;
 RA Kalamaraki P., Gazzotti P.;
 RT "Structural and functional characterization of the calmodulin and
 calpain binding domains of rat liver alphaII spectrin.";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

SEQUENCE FROM N A
 TISSUE: Skeletal;
 Zhou D., Urselli J.A., Porter N.C., Randall W.R., Bloch R.J.;
 "Expressional cloning of alpha fodrin from rat skeletal muscle";
 Submitted (AUG-1998) to the EMBL/GenBank/DBP databases.
 [1]
 RN SEQUENCE OF 1292 2321 FROM N.A.
 RS TISSUE: Kidney;
 RX MEDLINE-8937337; PubMed 276988;
 RA Bond W., Doyle D.;
 "Cloning and analysis of cDNA clones for rat kidney alpha-spectrin";
 J. Biol. Chem. 264:12759-12764(1989)
 CC 1- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
 INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
 THIS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
 CYTOSKELETON AT THE MEMBRANE (By similarity).
 CC 1- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 TETRAMERS.
 CC 1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC 1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC 1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC 1- SIMILARITY: CONTAINS 24 SPECTRIN REPEATS.
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR EMBL: X50845; CAA62350.1; .
 DR EMBL: AF084186; AAC34127.1; .
 DR EMBL: J04828; AAA40770.1; .
 DR PIR: A32612; A42612.
 DR HSRP: P07751; IAJ3.
 DR InterPro: IPR02048; EF-hand.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR02017; Spectrin.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00435; spectrin; 33.
 DR SMART: SM00054; Eph; 2.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00150; SPECT; 29.
 DR PROSITE: PS00018; EF_HAND; 2.
 DR PROSITE: PS50002; SH3; 1.
 KW Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
 Capping protein; Calcium-binding; Repeat; SH3 domain.
 FT REPEAT 10 42 SPECTRIN 1.
 FT REPEAT 44 147 SPECTRIN 2.
 FT REPEAT 149 253 SPECTRIN 3.
 FT REPEAT 255 359 SPECTRIN 4.
 FT REPEAT 361 465 SPECTRIN 5.
 FT REPEAT 467 571 SPECTRIN 6.
 FT REPEAT 573 676 SPECTRIN 7.
 FT REPEAT 678 782 SPECTRIN 8.
 FT REPEAT 784 888 SPECTRIN 9.
 FT REPEAT 890 955 SPECTRIN 10.
 FT DOMAIN 967 1026 SH3.
 FT REPEAT 1062 1089 SPECTRIN 11.
 FT REPEAT 1091 1161 SPECTRIN 12.
 FT REPEAT 1208 1241 SPECTRIN 13.
 FT REPEAT 1243 1337 SPECTRIN 14.
 FT REPEAT 1349 1443 SPECTRIN 15.
 FT REPEAT 1445 1549 SPECTRIN 16.
 FT REPEAT 1551 1656 SPECTRIN 17.
 FT REPEAT 1658 1762 SPECTRIN 18.
 FT REPEAT 1764 1868 SPECTRIN 19.
 FT REPEAT 1870 1974 SPECTRIN 20.
 FT REPEAT 1976 2081 SPECTRIN 21.
 FT REPEAT 2091 2195 SPECTRIN 22.

FT REPEAT 2205 2310 SPECTRIN 23.
 FT CA_BIND 2346 2347 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 2379 2390 EF_HAND 2 (POTENTIAL).
 FT CONFLICT 1329 1329 D > Y (IN REF. 3).
 FT CONFLICT 1514 1514 Y > L (IN REF. 1).
 FT CONFLICT 1702 1702 L > A (IN REF. 4).
 FT CONFLICT 1971 1972 K1 > NV (IN REF. 1).
 FT CONFLICT 2205 2206 K1 > NV (IN REF. 1).
 FT CONFLICT 2310 2321 SQIQAKNTTGV -- HADPQGEINRSII (IN REF. 4).
 SQ SEQUENCE 2472 AA: 284635 MW: 68000.02871278A CRC64:
 Query Match 61.7%; Score 37; DB 1; Length 2472;
 Best local Similarity 58.1%; Pred. No. 1.8e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Q7 1 EELMLRLQDYEE 12
 Db 969 KRLVIALDYDF 980
 :||:| | | | |
 RESULT 13
 SPQN_CHICK STANDARD; PRT: 2477 AA.
 AC P07751:
 DT 01 AUG 1988 (Rel. 08, Created)
 DI 01-AUG-1991 (Rel. 19, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
 DE (Fodrin alpha chain).
 DE (Fodrin alpha chain).
 GN SPIN1 OR SP1A2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89093238; PubMed-2910879;
 RA Wasenius V.-M., Saraste M., Salven P., Eraenaa M., Holm M.,
 Lehto V.-P.;
 RT "Primary structure of the brain alpha-spectrin";
 RL J. Cell Biol. 108:79-93(1989).
 RN 121
 RP REVISIONS.
 RA Wasenius V.-M., Saraste M., Salven P., Eraenaa M., Holm M.,
 Lehto V.-P.;
 RL J. Cell Biol. 108:1177-1178(1989).
 RN 131
 RP SEQUENCE OF 1695-2153 FROM N.A.
 RX MEDLINE-85284928; PubMed-4029118;
 RA Wasenius V.-M., Knowles J., Virtanen I., Lehto V.-P.;
 RT "Sequencing of the chicken non-erythroid spectrin cDNA reveals an
 internal repetitive structure homologous to the human erythrocyte
 spectrin";
 RL EMBO J. 4:1425-1430(1985).
 RN 141
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 945-1025.
 PX MEDLINE-93063299; PubMed-1279434;
 RA Musacchio A., Noble M., Pauplit R., Wierenga R., Saraste M.;
 PT "Crystal structure of a Src-homology 3 (SH3) domain";
 RL Nature 359:851-855(1992).
 RN 151
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 969-1025.
 RX MEDLINE-98363217; PubMed-9695637;
 RA Martinez J.C., Pisabarro M.T., Serrano L.;
 RT "Obligatory steps in protein folding and the conformational diversity
 of the transition state";
 RL Nat. Struct. Biol. 5:721-729(1998).
 RN 161
 RP STRUCTURE BY NMR OF 1763-1872.
 RX MEDLINE-98022917; PubMed-9356261;
 RA Pascual J., Pfuhl M., Walther D., Saraste M., Nilges M.;
 RT "Solution structure of the spectrin repeat: a left-handed

RT antiparallel triple-helical coiled-coil.";
 RL J. Mol. Biol. 273:740-751(1997).
 RN [7]
 RP STRUCTURE BY NMR OF 230-240.
 RX MEDLINE-96067121; PubMed-7580621;
 RA Trave G., Iacombe J. F., Ficht M., Saraste M., Pastore A.;
 RT "Molecular mechanism of the calcium induced conformational change in
 the spectrin EF-hands.";
 PL EMBO J. 14:4922-4931(1995).
 CC -1- FUNCTION: MOPHOGENETICALLY, SPECTPIN-LIKE PROTEINS APPEAR TO BE
 CC RELATED TO SPECTRIN, SHOWING A FLEXIBLE ROD-LIKE STRUCTURE.
 CC THEY CAN BIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULIN-
 CC BINDING ACTIVITY. IN NONERYTHROID TISSUES, SPECTRINS, IN
 CC ASSOCIATION WITH SOME OTHER PROTEINS, MAY PLAY AN IMPORTANT
 CC ROLE IN MEMBRANE ORGANIZATION.
 CC -1- SUBUNIT: LIKE EPYTHOCTE SPECTPIN, THE SPECTPIN-LIKE PROTEINS
 CC ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 CC Tetramers.
 CC -1- DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS:
 CC (1) N-TERMINAL DOMAIN (N),
 CC (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM),
 CC (3) MIDDLE DOMAIN (M),
 CC (4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC),
 CC (5) C-TERMINAL DOMAIN (C).
 CC NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES
 CC REPEATS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH
 CC OTHER. N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT
 CC FORM TYPICAL SPECTRIN REPEATS.
 CC -1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC
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 CC
 DR EMBL: X14518; CAA32662.1;
 DR EMBL: X14519; CAA32663.1; ACT_SEQ.
 DR PIR: X02593; CAA51571.1; ACT_SEQ.
 DR PIR: A30122; SUGHA.
 DR PDB: 1SHG; 31-OCT-93.
 DR PDB: 1AEY; 15-MAY-97.
 DR PDB: 1A33; 07-JUL-97.
 DR PDB: 1TUC; 01-AUG-96.
 DR PDB: 1TUD; 01-AUG-96.
 DR PDB: 1BK2; 16-FEB-99.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR000917; Spectrin
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00036; cfhnd; 2.
 DR Pfam: PF00435; spectrin; 23.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000012; EF-hand; 1.
 DR ProDom: PD000044; SH3; 1.
 DR SMART: SM00054; EFh; 2.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00150; SPC; 20.
 DR PROSITE: PS00018; EF-HAND; 2.
 DR PROSITE: PS00002; SH3; 1.
 KW Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
 KW Capping protein; Calcium-binding; Repeat; SH3 domain; 3D-structure.
 FT DOMAIN 1 14
 FT REPEAT 15 119
 FT REPEAT 120 225
 FT REPEAT 226 331
 FT REPEAT 332 437
 FT REPEAT 438 543
 FT REPEAT 544 648
 FT REPEAT 649 754

FT REPEAT 755 860
 FT REPEAT 861 966
 FT DOMAIN 967 1061
 FT SH3 1062 1256
 FT DOMAIN 1257 1362
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